

S.
Angari

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TECH

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/234,290B

Input Set : A:\10274-008003.txt
Output Set: N:\CRF4\06172003\I234290B.raw

4 <110> APPLICANT: Burkly, Linda C.
6 <120> TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES
9 <130> FILE REFERENCE: 10274-008003
11 <140> CURRENT APPLICATION NUMBER: US 09/234,290B
12 <141> CURRENT FILING DATE: 1999-01-20
14 <150> PRIOR APPLICATION NUMBER: US 08/447,118
15 <151> PRIOR FILING DATE: 1993-05-22
17 <150> PRIOR APPLICATION NUMBER: US 08/029,330
18 <151> PRIOR FILING DATE: 1993-02-09
20 <150> PRIOR APPLICATION NUMBER: PCT/US94/01456
21 <151> PRIOR FILING DATE: 1994-02-09
24 <160> NUMBER OF SEQ ID NOS: 19
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 360
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (0)...(0)
36 <223> OTHER INFORMATION: pBAG159 insert: HP1/2 heavy
37 chain variableregion; amino acid 1
38 is Glu (E) but Gln (Q) may be substituted
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)...(360)

ENTERED

W--> 44 <400> 1 48
45 gtc aaa ctg cag cag tct ggg gca gag ctt gtg aag cca ggg gcc tca
46 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser 15
47 1 5 10 15
49 gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc tat 96
50 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
51 20 25 30
53 atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att gga 144
54 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
55 35 40 45
57 agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc cag 192
58 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
59 50 55 60
61 gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg ctg 240
62 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
63 65 70 75 80
65 cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt gca 288
66 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/234,290B

DATE: 06/17/2003
TIME: 15:08:21

Input Set : A:\10274-008003.txt
Output Set: N:\CRF4\06172003\I234290B.raw

67	85	90	95	
69 gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc caa				336
70 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln				
71 100 105 110				
73 ggg acc acg gtc acc gtc tcc tca				360
74 Gly Thr Thr Val Thr Val Ser Ser				
75 115 120				
78 <210> SEQ ID NO: 2				
79 <211> LENGTH: 120				
80 <212> TYPE: PRT				
81 <213> ORGANISM: Homo sapiens				
83 <400> SEQUENCE: 2				
84 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser				
85 1 5 10 15				
86 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr				
87 20 25 30				
88 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly				
89 35 40 45				
90 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln				
91 50 55 60				
92 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu				
93 65 70 75 80				
94 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala				
95 85 90 95				
96 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln				
97 100 105 110				
98 Gly Thr Thr Val Thr Val Ser Ser				
99 115 120				
101 <210> SEQ ID NO: 3				
102 <211> LENGTH: 318				
103 <212> TYPE: DNA				
104 <213> ORGANISM: Homo sapiens				
106 <220> FEATURE:				
107 <221> NAME/KEY: misc_feature				
108 <222> LOCATION: (0)...(0)				
109 <223> OTHER INFORMATION: pBAG172 insert: HP1/2				
110 light chain variable region				
113 <221> NAME/KEY: CDS				
114 <222> LOCATION: (1)...(318)				
115 <223> OTHER INFORMATION: HP1/2 light chain variable region				
w--> 118 <400> 3				
119 agt att gtg atg acc cag act ccc aaa ttc ctg ctt gtt tca gca gga				48
120 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly				
121 1 5 10 15				
123 gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat				96
124 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp				
125 20 25 30				
127 gta gct tgg tac caa cag cca ggg cag tct cct aaa ctg ctg ata				144
128 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				

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129	35	40	45	
131	tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc			192
132	Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly			
133	50	55	60	
135	agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct			240
136	Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala			
137	65	70	75	80
139	gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac			288
140	Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr			
141	85	90	95	
143	acg ttc gga ggg ggg acc aag ctg gag atc			318
144	Thr Phe Gly Gly Thr Lys Leu Glu Ile			
145	100	105		
148	<210> SEQ ID NO: 4			
149	<211> LENGTH: 106			
150	<212> TYPE: PRT			
151	<213> ORGANISM: Homo sapiens			
153	<400> SEQUENCE: 4			
154	Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly			
155	1	5	10	15
156	Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp			
157	20	25	30	
158	Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile			
159	35	40	45	
160	Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly			
161	50	55	60	
162	Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala			
163	65	70	75	80
164	Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr			
165	85	90	95	
166	Thr Phe Gly Gly Thr Lys Leu Glu Ile			
167	100	105		
169	<210> SEQ ID NO: 5			
170	<211> LENGTH: 429			
171	<212> TYPE: DNA			
172	<213> ORGANISM: Homo sapiens			
174	<220> FEATURE:			
175	<221> NAME/KEY: CDS			
176	<222> LOCATION: (1)...(429)			
178	<221> NAME/KEY: sig_peptide			
179	<222> LOCATION: (1)...(57)			
W-->	181 <221> mat_peptide			
182	<222> LOCATION: (58)...(429)			
W-->	184 <221> misc_feature			
185	<222> LOCATION: (0)...(0)			
186	<223> OTHER INFORMATION: pBAG195 insert: AS heavy chain variable region			
W-->	189 <400> 5			
190	atg gac tgg acc tgg agg gtc ttc tgc ttg ctg gct gta gca cca ggt			48
191	Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly			

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TIME: 15:08:21

Input Set : A:\10274-008003.txt

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192	-15	-10	-5	
194	gcc cac tcc cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga			96
195	Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg			
196	1	5	10	
198	cct agc cag acc ctg agc ctg acc tgc acc gcg tct ggc ttc aac att			144
199	Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile			
200	15	20	25	
202	aaa gac acc tat atg cac tgg gtg aga cag cca cct gga cga ggt ctt			192
203	Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu			
204	30	35	40	45
206	gag tgg att gga agg att gat cct gcg agt ggc gat act aaa tat gac			240
207	Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp			
208	50	55	60	
210	ccg aag ttc cag gtc aga gtg aca atg ctg gta gac acc agc agc aac			288
211	Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn			
212	65	70	75	
214	cag ttc agc ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtc			336
215	Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val			
216	80	85	90	
218	tat tat tgt gca gac gga atg tgg gta tca acg gga tat gct ctg gac			384
219	Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp			
220	95	100	105	
222	tcc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gag tcc			429
223	Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser			
224	110	115	120	
227	<210> SEQ ID NO: 6			
228	<211> LENGTH: 143			
229	<212> TYPE: PRT			
230	<213> ORGANISM: Homo sapiens			
232	<220> FEATURE:			
233	<221> NAME/KEY: SIGNAL			
234	<222> LOCATION: (1)...(19)			
236	<400> SEQUENCE: 6			
237	Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly			
238	-15	-10	-5	
239	Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg			
240	1	5	10	
241	Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile			
242	15	20	25	
243	Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu			
244	30	35	40	45
245	Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp			
246	50	55	60	
247	Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn			
248	65	70	75	
249	Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val			
250	80	85	90	
251	Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp			
252	95	100	105	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/234,290B

DATE: 06/17/2003

TIME: 15:08:22

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

253 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
 254 110 115 120
 256 <210> SEQ ID NO: 7
 257 <211> LENGTH: 384
 258 <212> TYPE: DNA
 259 <213> ORGANISM: Homo sapiens
 261 <220> FEATURE:
 262 <221> NAME/KEY: CDS
 263 <222> LOCATION: (1)...(384)
 265 <221> NAME/KEY: sig_peptide
 266 <222> LOCATION: (1)...(57)
W--> 268 <221> mat_peptide
 269 <222> LOCATION: (58)...(384)
W--> 271 <221> misc_feature
 272 <222> LOCATION: (0)...(0)
 273 <223> OTHER INFORMATION: pBAG198 insert: VK (SVMDY) light chain variable
 274 region
W--> 277 <400> 7
 278 atg ggt tgg tcc tgc atc atc ctg ttc ctg gtt gct acc gct acc ggt 48
 279 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 280 -15 -10 -5
 282 gtc cac tcc agc atc gtg atg acc cag agc cca agc agc ctg agc gcc 96
 283 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 284 1 5 10
 286 agc gtg ggt gac aga gtg acc atc acc tgt aag gcc agt cag agt gtg 144
 287 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
 288 15 20 25
 290 act aat gat gta gct tgg tac cag cag aag cca ggt aag gct cca aag 192
 291 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 292 30 35 40 45
 294 ctg ctg atc tac tat gca tcc aat cgc tac act ggt gtg cca gat aga 240
 295 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
 296 50 55 60
 298 ttc agc ggt agc ggt tat ggt acc gac ttc acc ttc acc atc agc agc 288
 299 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 300 65 70 75
 302 ctc cag cca gag gac atc gcc acc tac tac tgc cag cag gat tat agc 336
 303 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
 304 80 85 90
 306 tct ccg tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgt aag 384
 307 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
 308 95 100 105
 311 <210> SEQ ID NO: 8
 312 <211> LENGTH: 128
 313 <212> TYPE: PRT
 314 <213> ORGANISM: Homo sapiens
 316 <220> FEATURE:
 317 <221> NAME/KEY: SIGNAL
 318 <222> LOCATION: (1)...(19)

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/234,290B

DATE: 06/17/2003

TIME: 15:08:23

Input Set : A:\10274-008003.txt

Output Set: N:\CRF4\06172003\I234290B.raw

L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:118 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:189 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:271 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:363 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:369 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:372 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:378 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:381 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9